

X12553.ST25.txt  
SEQUENCE LISTING

<110> Eli Lilly and Company  
<120> Erythropoietic Compounds  
<130> X-12553  
<140> US 09/856,451  
<141> 2001-05-22  
<150> PCT/US99/27801  
<151> 1999-11-23  
<160> 4  
<170> PatentIn version 3.2  
<210> 1  
<211> 168  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> synthetic construct  
  
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<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> Xaa at position 1 is absent or Met;  
  
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<222> (2)..(2)  
<223> Xaa at position 2 is absent or is Ala, Cys, Asp, Glu, Phe, Gly,  
His, Ile, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp, or Tyr  
  
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<222> (26)..(26)  
<223> Xaa at position 26 is Asn, Lys or Glu;  
  
<220>  
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<222> (40)..(40)  
<223> Xaa at position 40 is Asn, Lys or Glu;  
  
<220>  
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<222> (78)..(78)  
<223> Xaa at position 78 is Arg or Glu;  
  
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<222> (85)..(85)  
<223> Xaa at position 85 is Asn, Lys or Glu;  
  
<220>  
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<222> (90)..(90)  
<223> Xaa at position 90 is Trp, Lys, Pro, or Arg;  
  
<220>  
<221> MISC\_FEATURE  
<222> (128)..(128)  
<223> Xaa at position 128 is Ser, Thr, Lys or Glu;

<220>  
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 <222> (141)..(141)  
 <223> Xaa at position 141 is Arg or Glu;  
 <220>  
 <221> MISC\_FEATURE  
 <222> (156)..(156)  
 <223> Xaa at position 156 is Lys or Glu; and  
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 <222> (168)..(168)  
 <223> Xaa at position 168 is Arg, absent, or any other amino acid.

<400> 1

Xaa Xaa Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg  
 1 5 10 15

Tyr Leu Leu Glu Ala Lys Glu Ala Glu Xaa Ile Thr Thr Gly Cys Ala  
 20 25 30

Glu His Cys Ser Leu Asn Glu Xaa Ile Thr Val Pro Asp Thr Lys Val  
 35 40 45

Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu  
 50 55 60

Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Xaa Gly Gln  
 65 70 75 80

Ala Leu Leu Val Xaa Ser Ser Gln Pro Xaa Glu Pro Leu Gln Leu His  
 85 90 95

Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg  
 100 105 110

Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Xaa  
 115 120 125

Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Xaa Lys Leu Phe  
 130 135 140

Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Xaa Leu Tyr Thr Gly  
 145 150 155 160

Glu Ala Cys Arg Thr Gly Asp Xaa  
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<210> 2  
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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu  
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 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu  
 20 25 30  
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu  
 35 40 45  
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
 50 55 60  
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
 65 70 75 80  
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
 85 90 95  
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
 100 105 110  
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
 115 120 125  
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu  
 130 135 140  
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
 145 150 155 160  
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
 165 170 175  
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Arg

<210> 3  
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 gttccggaca ccaaagttaa cttctacgct tggaacgta tggaagttgg tcagcaggct 180  
 gttgaagttt ggcagggtct ggctctgctg tccgaagctg ttctgcgtgg tcaggctctg 240

X12553.ST25.txt

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 ggtctgcgtt ccctgaccac cctgctgcgt gctctgggtg ctcagaaaga agctatctcc 360  
 ccgccggacg ctgcttccgc tgctccgctg cgtaccatca ccgctgacac cttccgtaaa 420  
 ctgttccgtg tttactccaa cttcctgcgt ggtaaactga aactgtacac cggtgaagct 480  
 tgccgtaccg gtgactga 498

<210> 4  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic construct

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Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu  
 1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His  
 20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe  
 35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp  
 50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu  
 65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp  
 85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu  
 100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala  
 115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val  
 130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala  
 145 150 155 160

Cys Arg Thr Gly Asp  
 165